

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/470,735DATE: 06/13/96
TIME: 14:57:44

INPUT SET: S11056.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

 #7

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Israeli, Ron S.
Heston, Warren D.W.
Fair, William R.

(ii) TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States of America
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM 330 466 DX2
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/470,735
(B) FILING DATE: 06-JUN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 1747/41426-D

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2653 base pairs
(B) TYPE: nucleic acid

RAW SEQUENCE LISTING PATENT APPLICATION US/08/470,735

DATE: 06/13/96
TIME: 14:57:46

INPUT SET: S11056.raw

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47      (C) STRANDEDNESS: double
48      (D) TOPOLOGY: linear
49
50      (ii) MOLECULE TYPE: cDNA
51
52      (iii) HYPOTHETICAL: NO
53
54      (iv) ANTI-SENSE: NO
55
56      (vi) ORIGINAL SOURCE:
57          (A) ORGANISM: Homo sapiens
58          (F) TISSUE TYPE: Carcinoma
59
60      (vii) IMMEDIATE SOURCE:
61          (B) CLONE: Prostate-Specific Membrane Antigen
62
63      (ix) FEATURE:
64          (A) NAME/KEY: CDS
65          (B) LOCATION: 262..2511
66
67
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70      CTCAAAAGGG GCCGGATTTC CTTCTCCTGG AGGCAGATGT TGCCTCTCTC TCTCGCTCGG      60
71
72      ATTGGTTCAG TGCACTCTAG AAACACTGCT GTGGTGGAGA AACTGGACCC CAGGTCTGGA      120
73
74      GCGAATTCCA GCCTGCAGGG CTGATAAGCG AGGCATTAGT GAGATTGAGA GAGACTTTAC      180
75
76      CCCGCCGTGG TGGTTGGAGG GCGCGCAGTA GAGCAGCAGC ACAGGCGCGG GTCCCCGGGAG      240
77
78      GCCGGCTCTG CTCGCGCCGA G ATG TGG AAT CTC CTT CAC GAA ACC GAC TCG      291
79                               Met Trp Asn Leu Leu His Glu Thr Asp Ser
80                               1           5           10
81
82      GCT GTG GCC ACC GCG CGC CGC CCG CGC TGG CTG TGC GCT GGG GCG CTG      339
83      Ala Val Ala Thr Ala Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu
84                               15           20           25
85
86      GTG CTG GCG GGT GGC TTC TTT CTC CTC GGC TTC CTC TTC GGG TGG TTT      387
87      Val Leu Ala Gly Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe
88                               30           35           40
89
90      ATA AAA TCC TCC AAT GAA GCT ACT AAC ATT ACT CCA AAG CAT AAT ATG      435
91      Ile Lys Ser Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met
92                               45           50           55
93
94      AAA GCA TTT TTG GAT GAA TTG AAA GCT GAG AAC ATC AAG AAG TTC TTA      483
95      Lys Ala Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu
96      60           65           70
97
98      TAT AAT TTT ACA CAG ATA CCA CAT TTA GCA GGA ACA GAA CAA AAC TTT      531
99      Tyr Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/470,735

DATE: 06/13/96
TIME: 14:57:48

INPUT SET: S11056.raw

	75	80	85	90	
100					
101					
102	CAG CTT GCA AAG CAA ATT CAA TCC CAG TGG AAA GAA TTT GGC CTG GAT				579
103	Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp				
104		95	100	105	
105					
106	TCT GTT GAG CTA GCA CAT TAT GAT GTC CTG TTG TCC TAC CCA AAT AAG				627
107	Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys				
108		110	115	120	
109					
110	ACT CAT CCC AAC TAC ATC TCA ATA ATT AAT GAA GAT GGA AAT GAG ATT				675
111	Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile				
112		125	130	135	
113					
114	TTC AAC ACA TCA TTA TTT GAA CCA CCT CCT CCA GGA TAT GAA AAT GTT				723
115	Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val				
116		140	145	150	
117					
118	TCG GAT ATT GTA CCA CCT TTC AGT GCT TTC TCT CCT CAA GGA ATG CCA				771
119	Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser Pro Gln Gly Met Pro				
120	155	160	165	170	
121					
122	GAG GGC GAT CTA GTG TAT GTT AAC TAT GCA CGA ACT GAA GAC TTC TTT				819
123	Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe				
124		175	180	185	
125					
126	AAA TTG GAA CGG GAC ATG AAA ATC AAT TGC TCT GGG AAA ATT GTA ATT				867
127	Lys Leu Glu Arg Asp Met Lys Ile Asn Cys Ser Gly Lys Ile Val Ile				
128		190	195	200	
129					
130	GCC AGA TAT GGG AAA GTT TTC AGA GGA AAT AAG GTT AAA AAT GCC CAG				915
131	Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Lys Val Lys Asn Ala Gln				
132		205	210	215	
133					
134	CTG GCA GGG GCC AAA GGA GTC ATT CTC TAC TCC GAC CCT GCT GAC TAC				963
135	Leu Ala Gly Ala Lys Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr				
136		220	225	230	
137					
138	TTT GCT CCT GGG GTG AAG TCC TAT CCA GAT GGT TGG AAT CTT CCT GGA				1011
139	Phe Ala Pro Gly Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly				
140	235	240	245	250	
141					
142	GGT GGT GTC CAG CGT GGA AAT ATC CTA AAT CTG AAT GGT GCA GGA GAC				1059
143	Gly Gly Val Gln Arg Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp				
144		255	260	265	
145					
146	CCT CTC ACA CCA GGT TAC CCA GCA AAT GAA TAT GCT TAT AGG CGT GGA				1107
147	Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly				
148		270	275	280	
149					
150	ATT GCA GAG GCT GTT GGT CTT CCA AGT ATT CCT GTT CAT CCA ATT GGA				1155
151	Ile Ala Glu Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly				
152		285	290	295	

INPUT SET: S11056.raw

153																		
154	TAC	TAT	GAT	GCA	CAG	AAG	CTC	CTA	GAA	AAA	ATG	GGT	GGC	TCA	GCA	CCA		1203
155	Tyr	Tyr	Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro		
156		300					305					310						
157																		
158	CCA	GAT	AGC	AGC	TGG	AGA	GGA	AGT	CTC	AAA	GTG	CCC	TAC	AAT	GTT	GGA		1251
159	Pro	Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly		
160	315					320					325					330		
161																		
162	CCT	GGC	TTT	ACT	GGA	AAC	TTT	TCT	ACA	CAA	AAA	GTC	AAG	ATG	CAC	ATC		1299
163	Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile		
164					335					340					345			
165																		
166	CAC	TCT	ACC	AAT	GAA	GTG	ACA	AGA	ATT	TAC	AAT	GTG	ATA	GGT	ACT	CTC		1347
167	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu		
168				350					355					360				
169																		
170	AGA	GGA	GCA	GTG	GAA	CCA	GAC	AGA	TAT	GTC	ATT	CTG	GGA	GGT	CAC	CGG		1395
171	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg		
172			365					370					375					
173																		
174	GAC	TCA	TGG	GTG	TTT	GGT	GGT	ATT	GAC	CCT	CAG	AGT	GGA	GCA	GCT	GTT		1443
175	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val		
176		380					385					390						
177																		
178	GTT	CAT	GAA	ATT	GTG	AGG	AGC	TTT	GGA	ACA	CTG	AAA	AAG	GAA	GGG	TGG		1491
179	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp		
180	395					400					405					410		
181																		
182	AGA	CCT	AGA	AGA	ACA	ATT	TTG	TTT	GCA	AGC	TGG	GAT	GCA	GAA	GAA	TTT		1539
183	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe		
184					415					420					425			
185																		
186	GGT	CTT	CTT	GGT	TCT	ACT	GAG	TGG	GCA	GAG	GAG	AAT	TCA	AGA	CTC	CTT		1587
187	Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu		
188				430					435					440				
189																		
190	CAA	GAG	CGT	GGC	GTG	GCT	TAT	ATT	AAT	GCT	GAC	TCA	TCT	ATA	GAA	GGA		1635
191	Gln	Glu	Arg	Gly	Val	Ala												

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INPUT SET: S11056.raw

206	AGT GGC ATG CCC AGG ATA AGC AAA TTG GGA TCT GGA AAT GAT TTT GAG	1827
207	Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu	
208	510 515 520	
209		
210	GTG TTC TTC CAA CGA CTT GGA ATT GCT TCA GGC AGA GCA CGG TAT ACT	1875
211	Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr	
212	525 530 535	
213		
214	AAA AAT TGG GAA ACA AAC AAA TTC AGC GGC TAT CCA CTG TAT CAC AGT	1923
215	Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser	
216	540 545 550	
217		
218	GTC TAT GAA ACA TAT GAG TTG GTG GAA AAG TTT TAT GAT CCA ATG TTT	1971
219	Val Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe	
220	555 560 565 570	
221		
222	AAA TAT CAC CTC ACT GTG GCC CAG GTT CGA GGA GGG ATG GTG TTT GAG	2019
223	Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Gly Met Val Phe Glu	
224	575 580 585	
225		
226	CTA GCC AAT TCC ATA GTG CTC CCT TTT GAT TGT CGA GAT TAT GCT GTA	2067
227	Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val	
228	590 595 600	
229		
230	GTT TTA AGA AAG TAT GCT GAC AAA ATC TAC AGT ATT TCT ATG AAA CAT	2115
231	Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser Met Lys His	
232	605 610 615	
233		
234	CCA CAG GAA ATG AAG ACA TAC AGT GTA TCA TTT GAT TCA CTT TTT TCT	2163
235	Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser	
236	620 625 630	
237		
238	GCA GTA AAG AAT TTT ACA GAA ATT GCT TCC AAG TTC AGT GAG AGA CTC	2211
239	Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu	
240	635 640 645 650	
241		
242	CAG GAC TTT GAC AAA AGC AAC CCA ATA GTA TTA AGA ATG ATG AAT GAT	2259
243	Gln Asp Phe Asp Lys Ser Asn Pro Ile Val Leu Arg Met Met Asn Asp	
244	655 660 665	
245		
246	CAA CTC ATG TTT CTG GAA AGA GCA TTT ATT GAT CCA TTA GGG TTA CCA	2307
247	Gln Leu Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro	
248	670 675 680	
249		
250	GAC AGG CCT TTT TAT AGG CAT GTC ATC TAT GCT CCA AGC AGC CAC AAC	2355
251	Asp Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn	
252	685 690 695	
253		
254	AAG TAT GCA GGG GAG TCA TTC CCA GGA ATT TAT GAT GCT CTG TTT GAT	2403
255	Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp	
256	700 705 710	
257		
258	ATT GAA AGC AAA GTG GAC CCT TCC AAG GCC TGG GGA GAA GTG AAG AGA	2451